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OM nucleic - nucleic search, using sw model

Run on: September 10, 2002, 19:42:15 (Search time 2002.99 Seconds

(without alignments) 6149.166 Million cell updates/sec

Title: US-09-597-771-11

Perfect score: 780

Sequence: 1 aaagaatcctagagagagaa.....gcataaaaaaaaaaaaaa 780

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: gb\_da:\*  
2: gb\_hlg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*  
15: em\_da:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*  
29: em\_vi:\*  
30: em\_hlg\_hum:\*  
31: em\_hlg\_inv:\*  
32: em\_hlg\_other:\*  
33: em\_hlgo\_inv:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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1	780	100.0	780	6	AX068851	AX068851 Sequence
2	765	98.1	779	8	AF296084	AF296084 Lycopersi
3	640.4	82.1	733	8	AB004824	AB004824 Solanum t
4	396	50.8	632	8	AB004827	AB004827 Solanum t
5	386.2	49.5	760	8	AF296086	AF296086 Lycopersi
6	385.4	49.4	716	8	AB004823	AB004823 Solanum t
7	349.6	44.8	925	8	AF232604	AF232604 Manihot e
8	349.6	44.8	1288	8	AF266464	AF266464 Manihot e
9	343.8	42.4	1124	8	NP001752	NP001752 Lycopersi
10	330.8	42.1	713	8	AF296085	AF296085 Lycopersi
11	328.4	42.1	726	8	AB004825	AB004825 Solanum t
12	319.8	41.0	649	8	AF416338	AF416338 Medicago
13	318.6	40.8	725	8	AF252297	AF252297 Euphorbia
14	313.8	40.2	688	8	AB004826	AB004826 Solanum t
15	309.8	39.7	810	8	AF296081	AF296081 Lycopersi
16	309.8	39.7	812	6	AX068853	AX068853 Sequence
17	307.6	39.4	741	8	MS01F4DMR	MS01F4DMR Lycopersi
18	305.4	39.2	722	8	OS4252135	OS4252135 Oryza sat
19	302.6	38.8	715	8	AF296083	AF296083 Lycopersi
20	300	38.5	480	8	SYE238624	SYE238624 Senecio v
21	298.6	38.3	676	8	AY063780	AY063780 Arabidops
22	298.6	38.3	702	6	AX068855	AX068855 Sequence
23	298.6	38.3	702	8	AF296082	AF296082 Arabidops
24	297.4	38.1	807	8	ZMR1R1F5A	ZMR1R1F5A Arabidops
25	292.4	37.5	822	8	AF094773	AF094773 Oryza sat
26	288.8	37.0	676	8	AF372933	AF372933 Arabidops
27	288.6	36.7	831	8	AF034943	AF034943 Zea mays
28	286.6	36.7	765	8	AY039588	AY039588 Arabidops
29	283.8	36.4	480	8	AY055789	AY055789 Arabidops
30	283.8	36.4	702	8	NP001751A	NP001751A N. plumbagin
31	282.2	36.2	477	8	AY060530	AY060530 Arabidops
32	182.2	23.4	433	8	RIC225	RIC225 Arabidops
33	165.4	21.2	2156	8	YSCANBI	YSCANBI Arabidops
34	165.4	21.2	2472	8	SCYR047C	SCYR047C Arabidops
35	165.4	21.2	2538	8	SCHYPL	SCHYPL Arabidops
36	165.4	21.2	42500	8	YSC0TGMS	YSC0TGMS Arabidops
37	163.8	21.0	745	8	YSC0TF51B	YSC0TF51B Arabidops
38	162.2	20.8	167764	2	AP004303	AP004303 Oryza sat
39	161	20.6	199551	2	AC006281	AC006281 Plasmid
40	159.4	20.4	1053	3	AF109731	AF109731 Spodopter
41	158.2	20.3	1050	3	AF109730	AF109730 Spodopter
42	154	19.7	474	6	AX001142	AX001142 Sequence
43	154	19.7	738	8	YSC0TF5A	YSC0TF5A Arabidops
44	154	19.7	1394	8	YSC0TF5A	YSC0TF5A Arabidops
45	154	19.7	1923	8	SCHYPL2	SCHYPL2 Arabidops

## ALIGNMENTS

RESULT 1  
LOCUS AX068851  
DEFINITION Sequence 11 from Patent WO0102592.  
ACCESSION AX068851  
VERSION AX068851.1 GI:12578704  
KEYWORDS  
SOURCE  
ORGANISM

tomato.  
Lycopersicon esculentum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;  
Lycopersicon.  
1 (bases 1 to 780)  
REFERENCE  
AUTHORS Thompson,J.E., Wang,T.W. and Lu,D.L.  
TITLE Dna encoding a plant deoxyhypusine synthase, a plant eukaryotic  
initiation factor 5a, transgenic plants and a method for  
controlling senescence and programmed cell death in plants  
JOURNAL Patent: WO 0102592-A 13 11-JAN-2001,  
Senesco, Inc. (US)  
FEATURES  
source  
1..780  
/organism="Lycopersicon esculentum"



Db 361 GAAAGTGAACACCAAGATGACCTGAGCTTCCACCGATGATAAAATCTGCTGAAGCAG 420  
Qy 421 gttaaagatgggttcccaagaaagaaagatcttgatgctgtatgctgcgatgagc 480  
Db 421 GTTAAAGATGGGTCCAGGAAGAAAGATCTTGCTGTCTTATGCTCGAATGGC 480  
Qy 481 gaagagcaaatcaagccgttaagatgctgtgacaaagaataagtaatgtaagcagc 540  
Db 481 GAAGACCAATTAACCGCTTAAGATGTTGGTACCAAGAAATGATATGATGACAC 540  
Qy 541 -ataactacatgcaagacttaagaacatcatcatcccaatgctgtaactatgataca 598  
Db 541 ATATATATCTGCCAAAGCTTTAAGACATTATCATATCTAATGCTGACTTGTGATATCA 600  
Qy 599 ctatgatatataactgttattatgtaactgctcgtcaacaaagaagaagaactgctgtat 658  
Db 601 CTGATTTATTAACCTGTGTTATTTGCACGTTCAAACAAAAGAAAGAAACCTGCTGTAT 660  
Qy 659 gactaagaagaatattgctgttgcttcttgacagacagttgaactatgtgaacttct 718  
Db 661 GGCTAGAGAAAGATTTGGCTTTGAGCTTTTGCACGACACAGTTGACATGATGTGAAATTC 720  
Qy 719 acttttttttttgggtaaaatctctgctgttaatgttctgcaaaaaaataaaaaa 777  
Db 721 ACTTTTGTGTTGGTAAATACTGCTCGTTAATGTTTGCACAAAAAATAAAAAA 779

RESULT 3  
AB004824 733 bp mRNA linear PLN 05-FEB-1999  
LOCUS Solanum tuberosum mRNA for eukaryotic initiation factor 5A3,  
DEFINITION complete cds.  
ACCESSION AB004824  
VERSION AB004824.1 GI:2225880  
KEYWORDS eukaryotic initiation factor 5A3.  
SOURCE Solanum tuberosum (cultivar:Irish Cobbler) developing microtuber  
microtuber cDNA to mRNA.  
ORGANISM Solanum tuberosum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asterales; euasterids I; Solanales; Solanales; Solanales; Solanaceae; Solanum.  
1 (bases 1 to 733)  
2 (sites)  
In:J.G., Fujino,K. and Kikuta,Y.  
Nucleotide sequence of five cDNAs (Accession Nos.  
AB004823-AB004827) encoding eukaryotic translation initiation  
factor 5A (eIF-5A) from potato (PGR97-147)  
Plant Physiol. 115, 864 (1997)  
location/Qualifiers  
1. 733  
/organism="Solanum tuberosum"  
/cultivar="Irish Cobbler"  
/db\_xref="taxon:4113"  
/tissue\_type="microtuber"  
/dev\_stage="developing microtuber"  
48..530  
/gene="eIF5A3"  
48..530  
/gene="eIF5A3"  
/codon\_start=1  
/product="eukaryotic initiation factor 5A3"  
/protein\_id="BA30877.1"  
/db\_xref="GI:2225881"  
/translation="MSDEHHFSSKADAGASKTYPQOACTIRKNGTYIKGPKCKVE  
VSTKTKGHHGAKHFAIDIFNGKLEIDIVPSHNCADVPVHNRTDYDLIDISGEV  
SLTLESNTKDLRLPTDESILKQVDPQEGKDLVVSAMSGEQLINAIKIDGTKN  
"

BASE COUNT 232 a 142 c 166 g 193 t  
ORIGIN  
Query Match 82.1% Score 640.4; DB 8; Length 733;  
Best Local Similarity 94.9%; Pred. No 7;le-149;  
Matches 685; Conservative 0; Mismatches 31; Indels 6; Gaps 2;  
Qy 11 agagagagaagaagaaatcctatagagagaagacatgctgcagaagaacacacattgagt 70  
Db 16 ACAGAGAGAAAGGAATCCTAGAGAGAGAAAGCATGTGGACGAGAAACACCAATTTGACT 75  
Qy 71 caaaggcagatctgctgctcctcaaaaacttccacagcagagcttggaacacccgtaaga 130  
Db 76 CAAGGCAATCTCTGCTCCAAAACCTTACCCACGCAAGCTGGAACACCTCCGTAAGA 135  
Qy 131 atggttacatcgttatcaaaagccgtccctcgaaggttgttgagctccactcaaaaa 190  
Db 136 ATGTTACATCGTATCAAAAGCGCTCCCTCAAGGTTGTTGAGGTCTCCACTTCAAAA 195  
Qy 191 ctggaaaacagcagacatctaatgtaacttctgggaattgacatttcaattgagaaga 250  
Db 196 CTGGAAAGCAGGACATGCTAAATGTCCTTGTGGCAATTCATTTTCATGCAAGAA 255  
Qy 251 aactggaagatacgtctccgtccctcccaaatgtgtgacacatgtaaccgtaccg 310  
Db 256 AACTCGAAGATATCGTTCATCCATCTCCACAAATTTGTGACGTCACATATGTAACCGTACC 315  
Qy 311 acatcatgctgattatatactctgaagatgttgtctcaactcttactgaaagtga 370  
Db 316 ACTATCAGCTGATGACATCTCTGAAGATGTTGTGCTCCCTTCTTACTGAAAGTGGAA 375  
Qy 371 acacaagaagatgactcagcgttcccaacgaatgaanaatcgtcgtgaagcaggttaaatg 430  
Db 376 ACACCAAGGATGACCTCCGGCTTCCACGATGAAGTCTGGAAGAGGTAAAGATG 435  
Qy 431 ggttccagaagaagaagatcttctgtgtgtgtgtatgctgcatgagggagaagcaga 490  
Db 436 GGTTCAGAGAAAGAAAGATCTGTGGTGTCTGTATGTTCTGGCAATGGGAAAGACACA 495  
Qy 491 ttaacgcgttaagagatgtgtacccaagaatagtaatgtatgtcagcaaat--aatcac 548  
Db 496 TTAATCCATTAAGGATTTGGTATCCAAAGATATGTTGTGGTGGACATCATTAATAC 555  
Qy 549 tgcacaagcttaagaacatatacatcttaattgttacttggatatactatgata 608  
Db 556 TGCCTGATTAATGATGATTAATTAATTAATGATGATGATGATGATGATGATGAT 615  
Qy 609 aactggttatttgcacgttcaacaaagaagaagaactgctgttaagctagaaga 668  
Db 616 ATCTGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 675  
Qy 669 agatattgcttgagcttcttgacagcagatgtaacatgtaagaatctacttttt 728  
Db 676 AGTATGGCTTTGAGCTTTTGACACAGCATGTTGAA---GTGAATTCCTACTTTATTT 731  
Qy 729 tt 730  
Db 732 AT 733

RESULT 4  
AB004827 632 bp mRNA linear PLN 05-FEB-1999  
LOCUS Solanum tuberosum mRNA for eukaryotic initiation factor 5A1,  
DEFINITION complete cds.  
ACCESSION AB004827  
VERSION AB004827.1 GI:2225886  
KEYWORDS eukaryotic initiation factor 5A1.  
SOURCE Solanum tuberosum (cultivar:Irish Cobbler) developing microtuber  
microtuber cDNA to mRNA.  
ORGANISM Solanum tuberosum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;



Best Local Similarity 85.0%; Pred. No. 1.9e-85;	
Matches 431; Conservative 0; Mismatches 76; Indels 0; Gaps 0;	
QY 43	atgtcggaaagaagaacaccattttaatgaatcaaaagcagatgctgtgtccccaacttc 102
Db 57	ATGTCGATGAAGAACACACCATTTTGAAGTCACAAAGTGATGCGTGCCCTCAAAAACCTTAC 116
QY 103	ccacagaacgtcggaaacccatccgtaagaatgtttatcatcgtttcaaaagccgtcccg 162
Db 117	CCTCAACAAGCTGGGACTTATTTGCAAGAGTGCTTATATAGTTATCAAAAGGCAAGACTTGC 176
QY 163	aaggttgttgaaggtcccaactcacaacactggaaacacagacatgctaaatgtaacttt 222
Db 177	AAGGTTGTTGAGAGTCTCCACTTCCAAAACGTGCAAGCAGCAGCATGCAAAATGTCACTTT 236
QY 223	gtggcaatgtgaattttaatbfgaaagaacactggagaatatcgctccgtccccaagt 282
Db 237	GGGGCAATCGACATTTTCAATGAAAGAAAGCTTGAAGATATTGTTCTTCATCCCAACAT 296
QY 283	tgtgatgtgccacatglttaaccgtaccgactacacacgcgtatgatcatctcgaagatgt 342
Db 297	TGTGATGTGCCACAGCATGTCATGCTACTACATACATCACTGATTGACATCTCTGAAGATGT 356
QY 343	ttgtctcaactcttactgaaagtggaaacacacaaagatgacctcgaagctccaccagt 402
Db 357	TTTGTCCTCTCTTCTTACGAAATGGAACACCAAAAGTGACCTCAGACTTCCACCGAT 416
QY 403	gaaaatcgtcgtgaacgaatgtaagaatggttccaaggaagaagatctgtgtgtct 462
Db 417	GACGCCCTGTTGACCAAGTTTAAAGTGTGATTGAGGAAGAAAGATCTGTGTGCT 476
QY 463	gttatgtctgcatbfggaaagacagacttaacgcggttaagaatgtttgtgtaacaaagt 522
Db 477	GTGATGTCTGCAGATGGGGAAGAGACAGATCTGTGCTGTGAAGACATTTGATACCAAGAC 536
QY 523	tagtatagtcatgycagcataactac 549
Db 537	TAGTTGCGCTCAATTCTGCAGCATTAAT 563
RESULT 7	
AF323604	925 bp mRNA linear PLN 22-FEB-2001
LOCUS	AF323604
DEFINITION	Manihot esculenta initiation factor eIF5-A mRNA, complete cds.
ACCESSION	AF323604
VERSION	AF323604.1 GI:13094962
KEYWORDS	.
SOURCE	Cassava.
ORGANISM	Manihot esculenta
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
	Rosidae; eucosids I; Malpighiales; Euphorbiaceae; Manihot.
REFERENCE	1 (bases 1 to 925)
AUTHORS	Reilly,K., Winter,M., Han,Y. and Beeching,J.
TITLE	Manihot esculenta translation initiation factor eIF5-A
REFERENCE JOURNAL	Unpublished
	2 (bases 1 to 925)
AUTHORS	Reilly,K., Winter,M., Han,Y. and Beeching,J.
TITLE	Direct Submission
REFERENCE JOURNAL	Submitted (22-NOV-2000) Biology and Biochemistry, University of
	Bath, Claverton Down, Bath BA2 7AY, UK
FEATURES	Location/Qualifiers
source	1..925
	/organism="Manihot esculenta"
	/db_xref="taxon:3983"
CDS	51..533
	/note="eukaryotic translation initiation factor; formerly
	eIF4D; post-translationally modified to contain hypusine"
	/codon_start=1
	/transl_except="(pos:204..206,aa:OTHER)
	/product="initiation factor eIF5-A"
	/protein_id="AK12100.1"
	/db_xref="GI:13094963"

misc\_feature 201..221 /note="GKHGAK; Region: conserved hypusination motif"  
BASE COUNT 305 a 161 c 203 g 256 t  
ORIGIN

Query Match 44.8%; Score 349.6; DB 8; Length 925;  
Best Local Similarity 79.8%; Pred. No. 1.5e-76;  
Matches 412; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

QY 31 agagagagaagcagtcgagcagaagaacacatttgagtcagaagcagatgctgccc 90  
DB 39 AGAAAAACGCTATCTCGGACGAGAACACCTTCGAGTCCAGACGCGATCCTGGAGCC 98  
QY 91 tcaaaacttccacagaagaagctggaaccatcgtaagaatggttacaatcgttaca 150  
DB 99 TCCAAAGACCTTCCACACAGCTGGTACCATTCGAGAAAGGCTACATCTTAATCAAG 158  
QY 151 ggcgcctccgcaagtgctgagctccacttcaaaactggaacacgagacatgct 210  
DB 159 AATCGTCCTCGCAAGGTTATGGAGTTTCAACATCAAAAGACGGAAACATGTCATGCT 218  
QY 211 aaatgcaacttggtgcaattgaacatttcaatggaagaacatggaagatcgttc 270  
DB 219 AAGTGCATTTGTTGGAAATGATATATTCATGCAATGCAAAAACTTGAAATTTTCTCT 278  
QY 271 tctcccaaatgttgatgtgacacatgttaaccgtacagctacagctgatatc 330  
DB 279 TCATCCACATGTGATGTTCTCATGTTCACCTGATTCAGTATTCAGTATTCATATC 338  
QY 331 tctgaagaatggtttgtctcacttcttactgaagtgaagaacacgaagatgacct 390  
DB 339 TCGAAGATGTTTGTGAGTCTTGTGACTGAAACTGGAACACCAAGACGATCTCAGG 398  
QY 391 ctcccaacgagtgaaaattctgtcgaagcaggttaagaatgggttccagaagaagat 450  
DB 399 CTTCACCAACCATGATAAATGCTCAGCCAGATTAAAGATGGGTTGCTTAAGGAGGAC 458  
QY 451 ctgtgtgctgtctgtatgtctgcagatggcgagaagacagatlaaacgcgttaaga 510  
DB 459 CTGCTAGTAGGCTCATGTCTGCAATGGGAGAGAGACGATATGTTCCCTTAAGCAT 518  
QY 511 gtiaccaagaatagttatgtatgtcatgagcagataatc 546  
DB 519 GGTCCTAAAAATTAAAGATGATGCTATAGCATTTAGC 554

RESULT 8  
AF266464 1288 bp mRNA linear PLN 24-MAY-2001  
LOCUS AF266464  
DEFINITION Manihot esculenta translation initiation factor 5A mRNA, complete cds.  
ACCESSION AF266464  
VERSION AF266464.1 GI:14193248  
KEYWORDS  
SOURCE .  
ORGANISM Manihot esculenta  
Manihot esculenta; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Magnoliophyta; eudicotyledons; core eudicots; rosidae; eurosids I; Malpighiales; Euphorbiaceae; Manihot.  
REFERENCE 1 (bases 1 to 1288)  
AUTHORS Reilly,K., Winter,M.J., Han,Y., Tohme,J. and Beeching,J.R.  
JOURNAL Cassava translation initiation factor 5A (elf-5A)  
TITLE Unpublished  
REFERENCE 2 (bases 1 to 1288)  
AUTHORS Reilly,K., Winter,M.J., Han,Y., Tohme,J. and Beeching,J.R.  
JOURNAL Direct Submission  
Submitted (11-MAY-2000) Biology and Biochemistry, University of Bath, Claverton Down, Bath BA2 7AT, UK

FEATURES  
source Location/Qualifiers  
1..1288  
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71..553  
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/protein\_id="AAK55848.1"  
/db\_xref="GI:14193249"  
/translation="MSDEHHFESKADAGASKTPPOAGTIRKNGYIVIKNPKYME  
VSTSKTGHGAKCHPVGIDIFNGKLEIDIVSSHNCDVPHNRTDYQILDISEGCV  
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BASE COUNT 428 a 222 c 293 g 345 t  
ORIGIN

Query Match 44.8%; Score 349.6; DB 8; Length 1288;  
Best Local Similarity 79.8%; Pred. No. 1.5e-76;  
Matches 412; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

QY 31 agagagagaagcagtcgagcagaagaacacatttgagtcagaagcagatgctgccc 90  
DB 59 AGAAAAACGCTATCTCGGACGAGAACACCTTCGAGTCCAGACGCGATCTGGAGCC 118  
QY 91 tcaaaacttccacagaagaagctggaaccatcgtaagaatggttacaatcgttaca 150  
DB 119 TCCAAAGACCTTCCACACAGCTGGTACCATTCGCAAGATGGCTTCATCAATCAAG 178  
QY 151 ggcgcctccgcaagtgctgagctccacttcaaaactggaacacgagacatgct 210  
DB 179 AATGTCCTCCGCAAGGTTATGGAGTTTCAACATCAAAAGACGGAAACATGTCATGCT 238  
QY 211 aaatgcaacttggtgcaattgaacatttcaatggaagaacatggaagatcgttc 270  
DB 239 AAGTGCATTTGTTGGAAATGATATATTCATGCAATGCAAAAACTTGAAATTTTCTCT 298  
QY 271 tctcccaaatgttgatgtgacacatgttaaccgtacagctacagctgatatc 330  
DB 299 TCATCCACATGTGATGTTCTCATGTTCACCTGATTCAGTATTCAGTATTCATATC 358  
QY 331 tctgaagaatggtttgtctcacttcttactgaagtgaagaacacgaagatgacct 390  
DB 359 TCTGAAGATGTTTGTGAGTCTTCTGACGTAACCTGGAACACCAAGACGATCTCAGG 418  
QY 391 ctcccaacgagtgaaaattctgtcgaagcaggttaagaatgggttccagaagaagat 450  
DB 419 CTTCACCAACCATGATAAATGCTCAGCCAGATTAAAGATGGGTTGCTTAAGGAGGAC 478  
QY 451 ctgtgtgctgtctgtatgtctgcagatggcgagaagacagatlaaacgcgttaaga 510  
DB 479 CTGCTAGTAGGCTCATGTCTGCAATGGGAGAGAGCGGATATGTTCCCTTAAGCAT 538  
QY 511 gtiaccaagaatagttatgtcatgagcagcagataatc 546  
DB 539 GGTCCTAAAAATTAAAGATGATGCTATAGCATTTAGC 574

RESULT 9  
NP051552 1224 bp mRNA linear PLN 13-FEB-1992  
LOCUS NP051552  
DEFINITION N. plumbaginifolia mRNA NeIF-5A2 for Initiation factor 5A(2).  
ACCESSION X63542  
VERSION X63542.1 GI:19701  
KEYWORDS hypusine-containing protein; initiation factor; translation initiation factor.  
SOURCE .  
ORGANISM Nicotiana plumbaginifolia  
Nicotiana plumbaginifolia; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.  
REFERENCE 1 (bases 1 to 1224)  
AUTHORS Chamot,D.D.

TITLE	JOURNAL	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES	source
Direct Submission	Submitted (13-Dec-1991)	D. Chamrot, Institute of Plant Physiology, University of Berne, Altenbergrain 21, CH- 3013 Berne, SWITZERLAND	2 (bases 1 to 1224)	Chamrot, D. and Kuhlmeier, C.	Differential expression of genes encoding the hypusine-containing translation initiation factor, eIF-5A, in tobacco	Nucleic Acids Res. 20 (4), 665-669 (1992)	92178957	See also X63541-3.
location/Qualifiers	1..1224							
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/tissue="leaf"								
<1..38								
39..518								
/gene="NeIF-5A2"								
39..518								
/gene="NeIF-5A2"								
/codon_start=1								
/product="eukaryotic initiation factor 5A (2)"								
/protein_id="CAA5104.1"								
/db_xref="GI:19702"								
/db_xref="SWISS-PROT:P24922"								
/translation="MSDEEHQESKADAGSKYPOQAQIRKNGHIVYVIRGCKVYEVSNGSKGHAKCHPAIDIFFGKIEDIVPSSHNCDFVHVRNTDYLQILDISDFGVSLTLENSTKDDSLPDDNMLTQIKDGFAGKDLVVSVMANGEGICALKDIGPK"								
519..>1224								
345 a	261 c	229 g	389 t					
BASE COUNT								
ORIGIN								

Query Match	44.1%	Score 343.8	DB 8	Length 1224
Best Local Similarity	79.3%	Pred. No. 4.3e-75		
Matches 419	Conservative	0	Mismatches 107	Indels 1
				Gaps 1
QY 43	atgtcgacgaggaaccacatttgcattcaaggcagatgtgtgctctaaacattc	102		
Db 39	ATGTGGAACGGAGGACCCATTBTAGTCAAAAGGCGGTGGCTCTTAAACCTTAC	98		
QY 103	ccacagcaagcttggaaacatccgttaagaatgtttacatcgttatacaaaagccgtccgc	162		
Db 99	CCCTCAACAGAGTGGTACCATCGTTAAGAACGTCACATCGTCATCAAAAGGCGTCCGCG	158		
QY 163	aaggttgtgtgagctccctcaattccaanaactcgtgaanaacacggacatgcctaattgcattt	222		
Db 159	AAGGTGTGGAAAGTCTCTACATCCAAAACCGAAAGCAGCGGTCTGCAAAATGTCTATTTT	218		
QY 223	gtggcaattgcatttccaatgtaagaagaactgtgaatatcgttccgtccctccacaat	282		
Db 219	GTCGCTATGTGACATCTTCACGTGAAAGAGCTTGAAGTATTTGTTCCCTCTTCACACAAAT	278		
QY 283	ttgtatgtgcacatgtttaaaccgtaccagatcatcagctatgtatgtatcctcgaagatggt	342		
Db 279	TGTGATGTGCCCAACGTTAATCGTACAGATATACAGCTTATGTGACATTTCTGGAAGATGGA	338		
QY 343	ttgttccacttcttactgaagtgtgaacaacaagaatgacactcaagctccaccagat	402		
Db 339	TTTGTGAGTGTGCTCACTGTGAATATGTATACACCAAGATGACCTTAAAGCTCTTACGTAT	398		
QY 403	gaaaatctgcgtgaagcaggttaaagatgggttccagaagaagaagaagatctgtgtgtct	462		
Db 399	GATTAACCTCCTTAAACAGATCAAGATGAAGATGGTTGCTGTAGGGAAGAAAGACCTTGTGTGCT	458		
QY 463	gttaagctgcgtatgggcgaagcagattaaagccgttaagaatgttgttgaacagaat	522		
Db 459	GTCATGTGACAGCAATGGGTGAAGACCAATTTGTGCCCTGAAGGATATTTGGTCCCAAGTA	517		
QY 523	tagttatgtcatgtgcagcatatcactcgtcaaaagctttaagacata	569		
Db 518	AATCTCTGATTTGGAGATTTGCTCGATGCGGAAGTCTTTACTACCTTA	564		

LOCUS	AF296085	713 bp	mRNA	linear	PLN 14-MAY-2001
DEFINITION	Lycopersicon esculentum eukaryotic translation initiation factor 5A-3 mRNA, complete cds.				
ACCESSION	AF296085				
VERSION	AF296085.1	GI:12407790			
KEYWORDS					
SOURCE	tomato.				
ORGANISM	Lycopersicon esculentum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;				
REFERENCE	1 (bases 1 to 713)				
AUTHORS	Wang,T.-W., Lu,L., Wang,D. and Thompson,J.E.				
TITLE	Isolation and Characterization of Senescence-Induced cDNAs Encoding Deoxyhsp26 Synthase and Eucaryotic Translation Initiation Factor 5A from Tomato				
JOURNAL	J. Biol. Chem. 276 (20), 17541-17549 (2001)				
PIBMED	11278418				
REFERENCE	2 (bases 1 to 713)				
AUTHORS	Wang,T.-W., Wang,D., Lu,L. and Thompson,J.E.				
TITLE	Direct Submission				
JOURNAL	Submitted (16-AUG-2000) Biology, University of Waterloo, Waterloo, ON N2L 3G1, Canada				
FEATURES					
Source	Location/Qualifiers				
	1..713				
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	/db_xref="taxon:4081"				
	52..531				
	/note="eIF-5A3"				
	/codon_start=1				
	/product="eukaryotic translation initiation factor 5A-3"				
	/protein_id="AAG3649.1"				
	/db_xref="gi:12407791"				
	/translation="MSDEHGFESKADAGASKTYPOOAGTIRKNGYIVIGRPCKVVEVSTKGTGHHGAKHFVAIDIFGKTKEDIVPSSNCDPVHNVDTDLIDISDFRVSLLDNKNTRKDLPLPDENLISLKGFABGRKLVYSVMSAMEBOIMALKDIGPR"				
BASE COUNT	195 a 135 c 155 g 228 t				
ORIGIN					
Query Match	42.4%; Score 330.8; DB 8; Length 713;				
Best Local Similarity	80.8%; Pred. No. 7.2e-72;				
Matches	386; Conservative 0; Mismatches 92; Indels 0; Gaps 0;				
42	catgtcgaagaagaacacacatttgagtcagaagcagatgctggtgcctcaaaaacttt	101			
51	CATGCTGACGAGGAGCATCAATTGAGCTCAAGGCTGATGCCGAGCATCAAAAACCTTA	110			
102	cccaagaagaacttgaaaccatccgfaagaatggttaacttggttatacaaggccgtccctg	161			
111	CCCTCAACAAAGCTGGTACTATTTCGTMAAAGGGTATATCGTCATCAAAAGGCCGTCATG	170			
162	caagtggttgaggtctccacttcaaaaacgcggaagaacagagacgtgtaaatgacatt	221			
171	CAAGTTGTGGAAGCTCTACATCCAAAACGTGGCAGCAGCGTACGCCCAATGTGCAATT	230			
222	tgtggcaattgacatttccaatgynaagaanaactgynaagatacglttccgtccccaaca	281			
231	CGTTGCTATTGACATCTCTACCTGCGGAAGAAGCTTGAGATATTGTCCTTCACACAA	290			
282	tttgatgattgccaatgtaacgttaacccgtacccgactatcagcttgatatactctgaagatg	341			
291	TTTGATATGTGCCCATGTTAATCGTACGATTATTCAGCTTATTGACATCTCTGGAAGATG	350			
342	ttttgctccacttcttaactgaagynagaacccaagaagatagactcaggtccccaacga	401			
351	ATTGTGTAGTGTGCTTACTTACATGATGTGTAACCCAGAGATACCTCAGGCTTCTTACTGA	410			
402	tgaaatctgcttgaaagcaggttaagaatgaggttccagaagaagaagatcttggtgttc	461			

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|||||
Db 411 TAAAAATCGCTTTCACATGATCAAGACGGGTTTCCAGAGGTAAGACCTCGTGTCTC 470
Qy 462 tgtatgtctgcgatgagcgaagagacatlaacgcgttaaggatgtgtaccacag 519
|||||
Db 471 TGTATGTCAGCTATGAGGTAAGAGACAGATTAATGCTTTGAAGGATATTGGCCCCAAG 528

RESULT 11
AB004825 726 bp mRNA linear PLN 05-FEB-1999
LOCUS Solanum tuberosum mRNA for eukaryotic Initiation factor 5A4,
DEFINITION complete cds.
ACCESSION AB004825
VERSION AB004825.1 GI:2225882
KEYWORDS eukaryotic initiation factor 5A4.
SOURCE Solanum tuberosum (cultivar:Irish Cobbler) developing microtuber
microtuber cDNA to mRNA.
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
REFERENCE 1 (bases 1 to 726)
AUTHORS In,J.G.
JOURNAL Direct Submission
Submitted (13-JUN-1997) Jun Gyo In, Hokkaido University, Faculty of
Agriculture, Department of Botany, Kita 9 Nishi 9, Kita-ku,
Sapporo, Hokkaido 060, Japan (E-mail:In@a2.hines.hokudai.ac.jp,
Tel:+81-11-706-2482, Fax:+81-11-706-2471)
2 (sites)
REFERENCE In,J.G., Fujino,K. and Kikuta,Y.
AUTHORS Nucleotide sequence of five cDNAs (Accession Nos.
TITLE AB004823-AB004827) encoding eukaryotic translation initiation
factor 5A (eIF-5A) from potato (PGR97-147)
JOURNAL Plant Physiol. 115, 864 (1997)
FEATURES
source location/Qualifiers
1..726
/organism="Solanum tuberosum"
/cultivar="Irish Cobbler"
/db_xref="taxon:4113"
/tissue_type="microtuber"
/dev_stage="developing microtuber"
44..523
/gene="eIF5A4"
44..523
/cds
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/codon_start=1
/product="eukaryotic initiation factor 5A4"
/protein_id="AAA20878.1"
/db_xref="GI:2225883"
/translation="MSDEHGFESKADAGASKTYPQAGTIRKSGYVIKRPCKVE
VSTSKTGHAKCHFVAIDIFGKLEIDIVPSHNCDDVPHNRTDYQLDISDGFV
SLTDNGSTWDKDLPLPTDLSLISOIKDGFAGKDLVVSVMAMGEQINALDKIGPK"

BASE COUNT 185 a 137 c 162 g 242 t

Query Match 42.1%; Score 328.4; DB 8; Length 726;
Best Local Similarity 80.1%; Pred. No. 2.8e-71;
Matches 386; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

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Qy 222 tttggaattgacatttcaatggaagaactggaagatcgtctccgccacaa 281
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Db 223 CGTTGCTATTGATATCTTCACTGAGAAAGCTGTGAGATATTGTCCTCTTCACAA 282
Qy 282 ttgtatgttgcacatglttaaccgtaccactacagctgatgabatctctgaagatg 341
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Db 283 TTGTGATGTGCCCATGTTAATCGCACAGATPATCAGTTATTGACATCTCGAAGATGG 342
Qy 342 tttgtctcacttcttaacgaaagtggaaacacacagatgacctcaccacga 401
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Db 343 ATTTGTGAGTCTGCTCCTCAGTCACATGATTAACACCAAGATGACCTTCCTACCGA 402
Qy 402 tgaaatctgtctgaagcaggtttaaagatggtccaggaaggaagatctgtgtc 461
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Db 403 TGAATGCTGCTTTCACAGATCAAGATGGGTTTGCTGAGGGTAAGACCTGTTGTTC 462
Qy 462 tgtatgtcgcgatgagcgaagagacatlaacgcgttaaggatgtgtaccacaa 521
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Db 463 TGTATGTCAGCTATGAGGTAAGAGACAGATTAATGCCCTGAAGATATTGGCCCCAAGTA 522
Qy 522 tc 523
Db 523 AT 524

RESULT 12
AF416338 649 bp mRNA linear PLN 03-OCT-2001
LOCUS Medicago sativa eukaryotic translation Initiation factor 5A-2 mRNA,
DEFINITION complete cds.
ACCESSION AF416338
VERSION AF416338.1 GI:15866586
KEYWORDS Medicago sativa.
SOURCE Medicago sativa.
ORGANISM Medicago sativa.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliae;
Medicago.
REFERENCE 1 (bases 1 to 649)
AUTHORS Winlocov,I.
TITLE Alfalfa translation initiation factor 5A-2 from salt tolerant
calus
JOURNAL unpublished
REFERENCE 2 (bases 1 to 649)
AUTHORS Winlocov,I.
TITLE Direct Submission
JOURNAL Submitted (31-AUG-2001) Plant Biology, Arizona State University,
Main Campus, PO Box 871601, Tempe, AZ 85287-1601, USA
FEATURES
source location/Qualifiers
1..649
/organism="Medicago sativa"
/strain="Regen S"
/db_xref="taxon:3879"
/tissue_type="calus"
/notes="salt tolerant cell line; grown continuously in 171
mM NaCl"
52..531
/codon_start=1
/product="eukaryotic translation Initiation factor 5A-2"
/protein_id="AAL10404.1"
/db_xref="GI:1386587"
/translation="MSDEHHEEPADAGASKTYPQAGTIRKNGYVIKSPCKVE
VSTSKTGHAKCHFVAIDIFGKLEIDIVPSHNCDDVPHNRTDYQLDISDGFV
SLTDNGSTWDKDLPLPTDLSLITQIKDGFADGKDLVVSVMAMGEOLICALDKIGPK"

BASE COUNT 197 a 114 c 140 g 198 t

Query Match 41.0%; Score 319.8; DB 8; Length 649;
Best Local Similarity 78.2%; Pred. No. 3.9e-69;

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	Matches	384;	Conservative	0;	Mismatches	107;	Indels	0;	Gaps	0;
OY	39	aagcagctgcgcgaagaacacacattttagtcgaagcagatgtcgtgcctcaaaaac	98							
Db	48	AATCATGTCGTGCGAAGAATCATCTTTGAACCCGCTGCCGATGGCGGAGCTCCAAAC	107							
OY	99	ttcccaagcagcgtctggaaccatccgtaagaatggtttacatcgtttacaagcgcgttc	158							
Db	108	CTACCCCTCAACGCGGTGGTACTATTCCGCAAGATGTTACATAGTCATCAAGTCCAGGCC	167							
OY	159	ctgcgaaggttgttggagctccacactcaaaaactgaaaaacgcagacatgtcctaattgtca	218							
Db	168	TTGCAGAGTTGTTGAGGTTTCTACTTCACAAAACAGAAAACCTGGACATGCAAACTGTCA	227							
OY	219	cttttggccaattgacatttcaatgagaagaagaactgtgaagatcattcgttcgtccca	278							
Db	228	CTTTGTTGCTATTGATATTTCATATGGGAAAAAATTGAAGATATTGTTCCTTATCCCA	287							
OY	279	caattgtatgtgccaacatggttaaccgtacccgactataagctgatltgatlatctctgaaga	338							
Db	288	CAATTGTATGTTCTCCACAGTCAACGTAACGTACATGATTATCAGTTGATGATATTTCGAGA	347							
OY	339	tgtgtttctcactcttactgaagaagtggaacacgaagatgacctcagcttccac	398							
Db	348	TGGATTTTGAGCTTTGTTGACTGACAAAGAGAGTCCAAAAGTGTCTGAAACCTTCCATAC	407							
OY	399	cgatgaaaaatcctgcgcgaagcaggttaagaatgtggttccaggaaggaagaactctgtgt	458							
Db	408	TGATGATTCACACTTACTCTACGATTTAAAGATGCGATTTCCTGATGAAAAAGATCTGTGCT	467							
OY	459	gtctgttatgtctgcgatgagcgaaagacagatlaacgcgcttlaagatgttctgaccaa	518							
Db	468	TTCTGTATATGTCGTGCGATGGGTGAAGACAGATATGTGCCCTGGAAGACATTGGTCTTAA	527							
OY	519	gaattagttat	529							
Db	528	GTAGTAATTTT	538							

FEATURES	source
LOCUS	AF225297 725 bp mRNA linear PLN 26-JAN-2000
DEFINITION	Euphorbia esula translation initiation factor 5A mRNA, partial cds.
ACCESSION	AF225297
VERSION	AF225297.1 GI:6752916
KEYWORDS	
SOURCE	
ORGANISM	leafy spurge. Euphorbia esula
REFERENCE	Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eustosids I; Malpighiales; Euphorbiaceae; Euphorbia. 1 (bases 1 to 725) Anderson, J.V. and Horvath, D.P. Identification of mRNAs expressed in underground adventitious buds of Euphorbia esula (leafy spurge) Unpublished 2 (bases 1 to 725) Anderson, J.V. and Horvath, D.P. Direct Submission Submitted (14-JAN-2000) Plant Science, USDA/ARS, 1605 Albrecht Blvd., Fargo, ND 58105, USA Location/Qualifiers 1..725
JOURNAL	
AUTHORS	
TITLE	
JOURNAL	
FEATURES	
source	
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CDS	

[illegible]

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source Location/Qualifiers  
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/cultivar="Irish Cobbler"  
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/dev\_stage="developing microtuber"  
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64..543  
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CDS  
64..543  
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/product="eukaryotic initiation factor 5A5"  
/protein\_id="BA20879.1"  
/db\_xref="GI:222585"  
/translation="MSDEHHFESSKADAGSKTYPOQAGTIRKSGHIVIKNRPCKYVE  
VSTSKTGHGKHAKEHFAIDIFNKKLEIDIVPSHNCDPVHNRDYOOLDIEDGFV  
SLTJENGNKDKLRLPTDPTLLAOKVKGFAEKGDIIVLSVMSAMGEQICGIRKIDGPK"

BASE COUNT 181 a 137 c 161 g 209 t

ORIGIN

Query Match 40.2%; Score 313.8; DB 8; Length 688;  
Best Local Similarity 77.9%; Pred. No. 1.2e-67;  
Matches 378; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

37 agaagcatgtcgcgcgaagaacacatlttgatcgaagcgaatgtcgtcctcaaa 96  
58 AAAAGATGTCGACGAGAGACACACTTGATTCAGAGCCAGCCGAGCTTCAAG 117  
97 acttccacagcaagctggaacatcgtlaagaatgttaccatcgttacaagccgt 156  
118 ACGTACCCCTACACAGCTGTGACTATCGTAAGAGTGTGCATCGCATCAAAAATCG 177  
157 cctcgcaagtgctgtgcgtcccaacttcaaaaacttgaagaacacggacatgtc 216  
178 CATTGCAAGGAGTGTGAAGTTTCACATTCACAGCAGCAAGCAGCGTCAATAATGT 237  
217 cacttctggaattgacatttcaatggaagaacactggaagatatcgtccgtctcc 276  
238 CACTTTGTGCAATTTGACATTTTCTACTGGAAGAGCTTGAAGTATTTGTTCCCTCTTC 297  
277 cacaattgtatgtgcacacatgttaacgtaacgtaacatcgtatgatactctgaa 336  
298 CACAATTGTGATGTTCCATGTAATAGACGTGATTAATGAGTTTATCTCTGAG 357  
337 gatgtgttctcacttctacttgaagtgtgaacacacgaagatgacctcaagctcc 396  
358 GATGGCTTTGTGACTTTGTGACTGAAAAATGCTAACACCAAGGTGACTTGAGGCTCCCA 417  
397 accgatgaataatctgcgtgaagcaggttaagaatgtgtccagaagaagaagaatctgtg 456  
418 ACTGATGATCTCTTCTTGCGCTCAAGGTCAAAAGATGTTTTCGCGAGGGAAGACCTGGTT 477  
457 gtgtctgtatctatctgtcgtatggtgcgaagacagataacgcgtttaaagctgtgtac 516  
478 CTGTCAGATGATGCTGCCATGGAGAGAGACGATTTGTGTATCAAGACATTTGGCCCT 537  
517 aagaa 521  
538 AAGTA 542

RESULT 15  
AF296081 810 bp mRNA linear PLN 14-MAY-2001  
LOCUS AF296081  
DEFINITION Dianthus caryophyllus eukaryotic translation initiation factor 5A  
ACCESSION AF296081  
VERSION AF296081.1 GI:12407782  
KEYWORDS  
SOURCE clove pink.  
ORGANISM Dianthus caryophyllus

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
PUBMED  
11278418  
2 (bases 1 to 810)  
REFERENCE  
Wang,T.-W., Wang,D., Lu,L. and Thompson,J.E.  
Isolation and Characterization of Senescence-Induced cDNAs Encoding  
Deoxyhypusine Synthase and Eukaryotic Translation Initiation Factor  
5A from Tomato  
J. Biol. Chem. 276 (20), 17541-17549 (2001)  
11278418  
2 (bases 1 to 810)  
REFERENCE  
Wang,T.-W., Wang,D., Lu,L. and Thompson,J.E.  
Direct Submission  
Submitted (16-AUG-2000) Biology, University of Waterloo, Waterloo,  
ON N2L 3G1, Canada  
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source Location/Qualifiers  
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/db\_xref="taxon:3570"  
67..549  
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CDS  
67..549  
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/protein\_id="AAG33645.1"  
/db\_xref="GI:12407783"  
/translation="MSDDHHFESSADAGSKTYPOQAGTIRKSGHIVIKNRPCKYVE  
VSTSKTGHGKHAKEHFAIDIFNKKLEIDIVPSHNCDPVHNRDYOOLDIEDGFV  
SLTJDSGDKDKLRLPDAELVYKMKRSGFEGKRLILSWCMAMGEEDICAVKXVSSGK"

BASE COUNT 232 a 152 c 192 g 234 t

ORIGIN

Query Match 39.7%; Score 309.8; DB 8; Length 810;  
Best Local Similarity 76.5%; Pred. No. 1.2e-66;  
Matches 380; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

29 ctagaagagacatgttcgcgcgaagaacacatlttgatcgaagcgaatgtcgtg 88  
53 CGAAAATGAGAGATGTCGACGAGACGATCACATTTGAGATCGCCGCGCGGAG 112  
89 cctcaaaaacttcccaagcagcgtggaacatcgcgaagaatgttaccatcgtatca 148  
113 CATCCAAGACTTACCCCTCAACAGCTGTGACTGACATTCGGAAGCGCTGACATCGCATCA 172  
149 aagcgctccctgcgcgaagtgctgtgcgtcccaacttcaaaaacttgaagaacacggacatg 208  
173 AAAATGCCCCCTGCAAGAGGTGAGGTTTCTACTCCAGACTGCGAAGCGGTCAATG 232  
209 ctaaatgtcacttctggaattgacatttcaatggaagaacactggaagatatcgttc 268  
233 CCAAAATGATCTTGTGTGCGATTTGACATTTCAACGGCAAGAGCTGGAATATTGTCC 292  
269 cgtctcccaacaatgtgtatgtgcacatgttaacccgtacacgactacatcgtatgtgta 328  
293 CCTCATCCCAACATTTGTGTTCCATGTCACCGTCCGTCACATPACACGCTTGATTA 352  
329 tctctgaagaatgttctgtcacttctcacttcaactgaagtgtgaagaacacgaagatgacctca 388  
353 TCACGTGAATATGCTTTGTGTACTCTGCTGACAGACAGTGTGCACACCAAGATGATCTGA 412  
389 ggtctcccaacaatctgtcgtgaagcaggttaagaatgtgttccagaagaagaag 448  
413 AGCTTCTCTGATGAGGCCCTTGTGAAGACAGATGAAGAGGATTTGAGCGGGAAG 472  
449 acctgtgtgtctgtatgtcgtatggtgcgaagcgaagcgaagcgaagcgttaagatg 508  
473 ACTTGATTTCTGACATGATGATGCAATGTGAGAGACGACATCTGCCCGCTCAAGGACG 532  
509 tctgtaccaagaattag 525  
533 TTAGTGTGTGCAAGTAG 549

Search completed: September 10, 2002, 21:43:05  
Job time: 7250 sec

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